Amendments to the Specification:

Please replace the paragraph (or section) beginning at page 1, line 5, with the following redlined paragraph (or section):

This application is a divisional of U.S. Patent Application No. 09/439,313, filed November 12, 1999, now Patent No. 6,329,505, which is a continuation-in-part of U.S. Patent Application No. 09/352,616, filed July 13, 1999, now Patent No. 6,395,278, which is a continuation-in-part of U.S. Patent Application No. 09/288,946, filed April 9, 1999, now abandoned, which is a continuation-in-part of U.S. Patent Application No. 09/232,149, filed January 15, 1999, now Patent No. 6,465,611~~, which is a continuation-in-part of U.S. Patent Application No. 09/159,812, filed September 23, 1998, which is a continuation-in-part of U.S. Patent Application No. 09/115,453, filed July 14, 1998, which is a continuation-in-part of U.S. Patent Application No. 09/030,607, filed February 25, 1998, which is a continuation-in-part of U.S. Patent Application No. 09/020,956, filed February 9, 1998, which is a continuation-in-part of U.S. Patent Application No. 08/904,804, filed August 1, 1997, which is a continuation-in-part of U.S. Patent Application No. 08/806,099, filed February 25, 1997~~.

Please replace the paragraph (or section) beginning at page 7, line 30, with the following redlined paragraph (or section):

Figure 8 illustrates the results of epitope mapping studies on P501S. The peptides used in the study are shown from left to right at the bottom of the figure, as follows: MDRLVQRPGTRAVYLASVA (SEQ ID NO: 489), YLASVAAFPVAAGATCLSHS (SEQ ID NO: 490), TCLSHSVAVVTASAALTGFT (SEQ ID NO: 491), ALTGFTFSALQILPYTLASL (SEQ ID NO: 492), YTLASLYHREKQVFLPKYRG (SEQ ID NO: 493), LPKYRGDTGGASSEDSLMIS (SEQ ID NO: 494), DSLMTSFLPGPKPGAPFPNG (SEQ ID NO: 495), APFPNGHVGAGGSGLLPPPPA (SEQ ID NO: 496), LLPPPPALCGASACDVSVRV (SEQ ID NO: 497), DVSVRVVVGEPTEARVVPGR (SEQ ID NO: 498), RVVPGRGICLDLAILDSAFL (SEQ ID NO: 499), LDSAFLLSQVAPSLFMGSIV (SEQ ID NO: 500), FMGSIVQLSQSVTAYMVSAA (SEQ ID NO: 501).

Please replace the paragraph (or section) beginning at page 8, line 1, with the following redlined paragraph (or section):

Figure 9 is a schematic representation of the P501S protein (SEQ ID NO:113) showing the location of transmembrane domains and predicted intracellular and extracellular domains.

Please insert the following paragraph beginning at page 9, line 6, with the following redlined paragraph:

Figure 11 shows the results of an ELISA assay to determine the specificity of rabbit polyclonal antisera raised against P501S. The depicted sequence corresponding to peptide P501S 306-320 is set forth in SEQ ID NO: 519 and the sequence corresponding to P501S 296-320 is set forth in SEQ ID NO: 520.

Please replace the paragraph (or section) beginning at page 31, line 29, with the following redlined paragraph (or section):

In certain instances, it is possible to obtain a full length cDNA sequence by analysis of sequences provided in an expressed sequence tag (EST) database, such as that available from ~~GenBank~~GENBANK™. Searches for overlapping ESTs may generally be performed using well known programs (*e.g.*, NCBI BLAST searches), and such ESTs may be used to generate a contiguous full length sequence. Full length DNA sequences may also be obtained by analysis of genomic fragments.

Please replace the paragraph (or section) beginning at page 68, line 13, with the following redlined paragraph (or section):

The cDNA sequences for the isolated clones were compared to known sequences in the gene bank using the EMBL and ~~GenBank~~ GENBANK™ databases (release 96). Four of the prostate tumor cDNA clones, F1-13, F1-16, H1-1, and H1-4, were determined to encode the

following previously identified proteins: prostate specific antigen (PSA), human glandular kallikrein, human tumor expression enhanced gene, and mitochondria cytochrome C oxidase subunit II. H1-9 was found to be identical to a previously identified human autonomously replicating sequence. No significant homologies to the cDNA sequence for F1-12 were found.

Please replace the paragraph (or section) beginning at page 71, line 3, with the following redlined paragraph (or section):

Additional studies with prostate subtraction spike 2 resulted in the isolation of three more clones. Their sequences were determined as described above and compared to the most recent ~~GenBank~~GENBANK™. All three clones were found to have homology to known genes, which are Cysteine-rich protein, KIAA0242, and KIAA0280 (SEQ ID NO: 317, 319, and 320, respectively). Further analysis of these clones by Synteni microarray (Synteni, Palo Alto, CA) demonstrated that all three clones were over-expressed in most prostate tumors and prostate BPH, as well as in the majority of normal prostate tissues tested, but low expression in all other normal tissues.

Please replace the paragraph (or section) beginning at page 80, line 1, with the following redlined paragraph (or section):

Further studies using a PCR-based subtraction library of a prostate tumor pool subtracted against a pool of normal tissues (referred to as JP: PCR subtraction) resulted in the isolation of thirteen additional clones, seven of which did not share any significant homology to known ~~GenBank~~ GENBANK™ sequences. The determined cDNA sequences for these seven clones (P711P, P712P, novel 23, P774P, P775P, P710P and P768P) are provided in SEQ ID NO: 307-311, 313 and 315, respectively. The remaining six clones (SEQ ID NO: 316 and 321-325) were shown to share some homology to known genes. By microarray analysis, all thirteen clones showed three or more fold over-expression in prostate tissues, including prostate tumors, BPH and normal prostate as compared to normal non-prostate tissues. Clones P711P, P712P, novel 23 and P768P showed over-expression in most prostate tumors and BPH tissues tested (n=29), and in the majority of normal prostate tissues (n=4), but background to low expression

levels in all normal tissues. Clones P774P, P775P and P710P showed comparatively lower expression and expression in fewer prostate tumors and BPH samples, with negative to low expression in normal prostate.

Please replace the paragraph (or section) beginning at page 80, line 27, with the following redlined paragraph (or section):

Using PCR and hybridization-based methodologies, additional cDNA sequence information was derived for two clones described above, 11-C9 and 9-F3, herein after referred to as P707P and P714P, respectively (SEQ ID NO: 333 and 334). After comparison with the most recent ~~GenBank~~GENBANK™, P707P was found to be a splice variant of the known gene HoxB13. In contrast, no significant homologies to P714P were found.

Please replace the paragraph (or section) beginning at page 84, line 1, with the following redlined paragraph (or section):

Additional studies using the PCR-based subtraction library consisting of a prostate tumor pool subtracted against a normal prostate pool (referred to as PT-PN PCR subtraction) yielded three additional clones. Comparison of the cDNA sequences of these clones with the most recent release of ~~GenBank~~ GENBANK™ revealed no significant homologies to the two clones referred to as P715P and P767P (SEQ ID NO: 312 and 314). The remaining clone was found to show some homology to the known gene KIAA0056 (SEQ ID NO: 318). Using microarray analysis to measure mRNA expression levels in various tissues, all three clones were found to be over-expressed in prostate tumors and BPH tissues. Specifically, clone P715P was over-expressed in most prostate tumors and BPH tissues by a factor of three or greater, with elevated expression seen in the majority of normal prostate samples and in fetal tissue, but negative to low expression in all other normal tissues. Clone P767P was over-expressed in several prostate tumors and BPH tissues, with moderate expression levels in half of the normal prostate samples, and background to low expression in all other normal tissues tested.

Please replace the paragraph (or section) beginning at page 97, line 20, with the following redlined paragraph (or section):

Potential prostate-specific genes present in the ~~GenBank~~ GENBANK™ human EST database were identified by electronic subtraction (similar to that described by Vasmatizis et al., *Proc. Natl. Acad. Sci. USA 95*:300-304, 1998). The sequences of EST clones (43,482) derived from various prostate libraries were obtained from the ~~GenBank~~GENBANK™ public human EST database. Each prostate EST sequence was used as a query sequence in a BLASTN (National Center for Biotechnology Information) search against the human EST database. All matches considered identical (length of matching sequence >100 base pairs, density of identical matches over this region > 70%) were grouped (aligned) together in a cluster. Clusters containing more than 200 ESTs were discarded since they probably represented repetitive elements or highly expressed genes such as those for ribosomal proteins. If two or more clusters shared common ESTs, those clusters were grouped together into a "supercluster," resulting in 4,345 prostate superclusters.

Please replace the paragraph (or section) beginning at page 97, line 20, with the following redlined paragraph (or section):

Records for the 479 human cDNA libraries represented in the ~~GenBank~~ GENBANK™ release were downloaded to create a database of these cDNA library records. These 479 cDNA libraries were grouped into three groups: Plus (normal prostate and prostate tumor libraries, and breast cell line libraries, in which expression was desired), Minus (libraries from other normal adult tissues, in which expression was not desirable), and Other (libraries from fetal tissue, infant tissue, tissues found only in women, non-prostate tumors and cell lines other than prostate cell lines, in which expression was considered to be irrelevant). A summary of these library groups is presented in Table II.